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Identifying predictable patterns in disease emergence

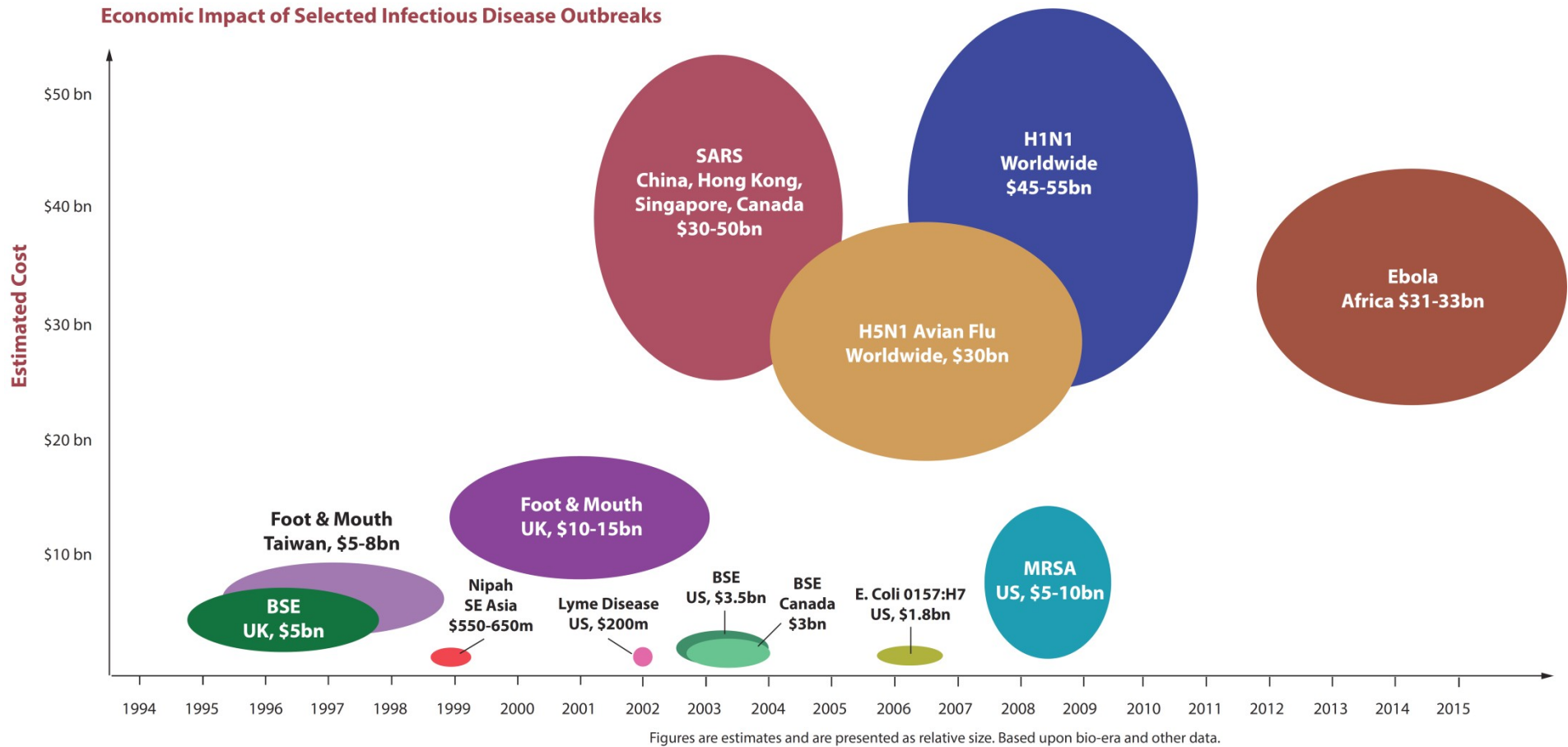
Peter Daszak
EcoHealth Alliance, New York, USA
www.ecohealthalliance.org



**Local conservation.
Global health.**



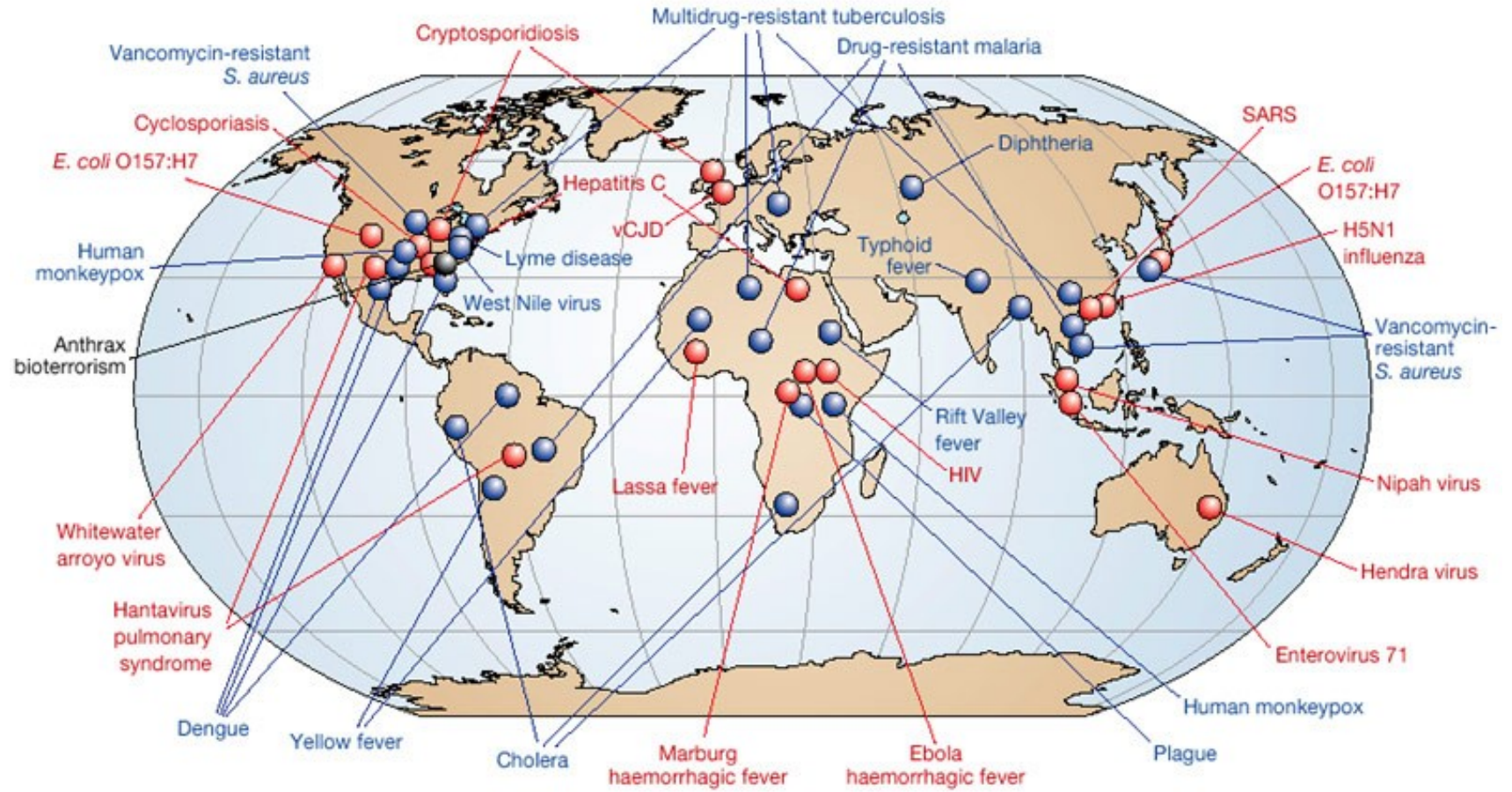
Economic Impact of Emerging Diseases



Local conservation.
Global health.



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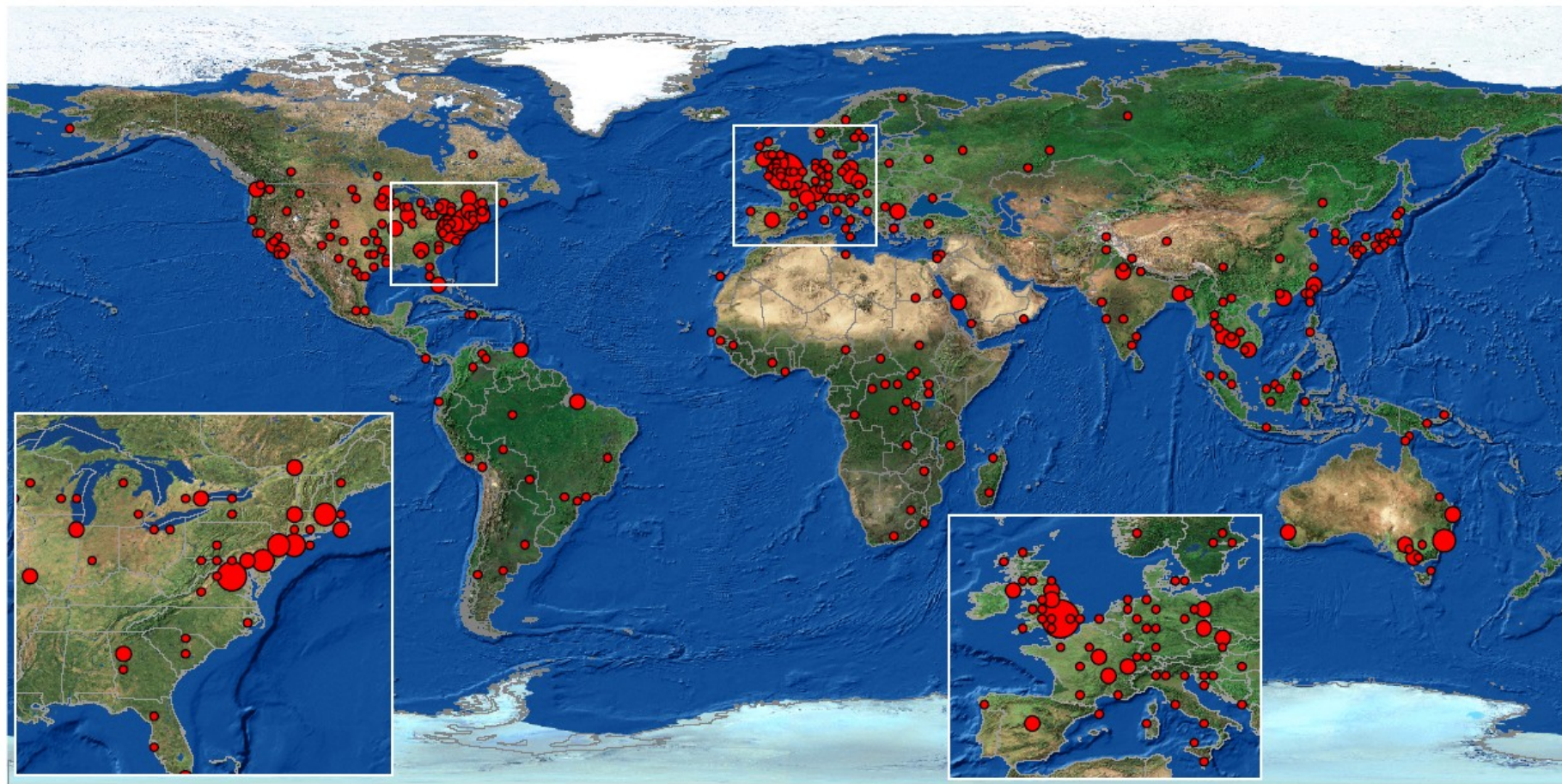
Local conservation.
Global health.

Fauci (2001) *Clin. Infect. Dis.*



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Total EID events • 1 • 2-3 • 4-5 • 6-7 • 8-11



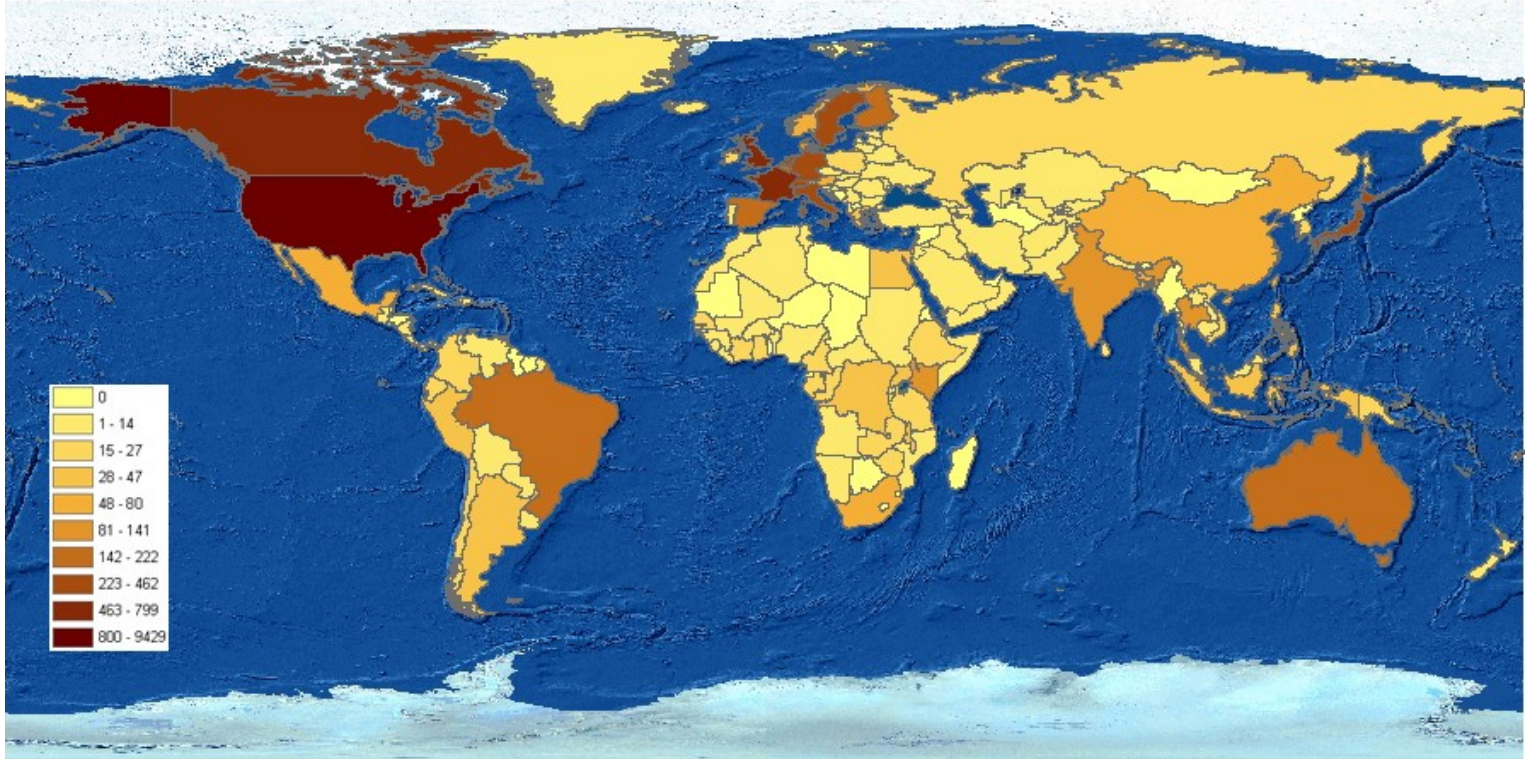
Local conservation.
Global health.

Jones *et al.* 2008 *Nature*



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Spatial reporting bias by country

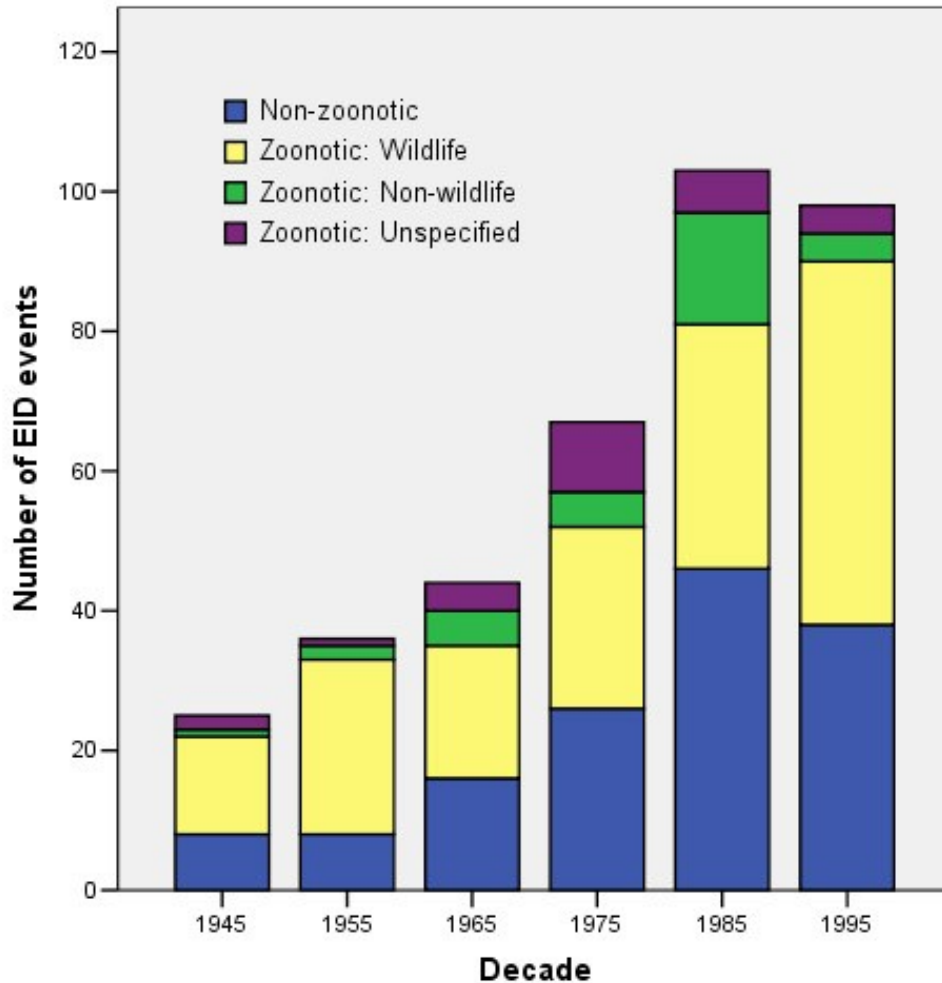


Each author's country from every *JID* paper 1973-2004

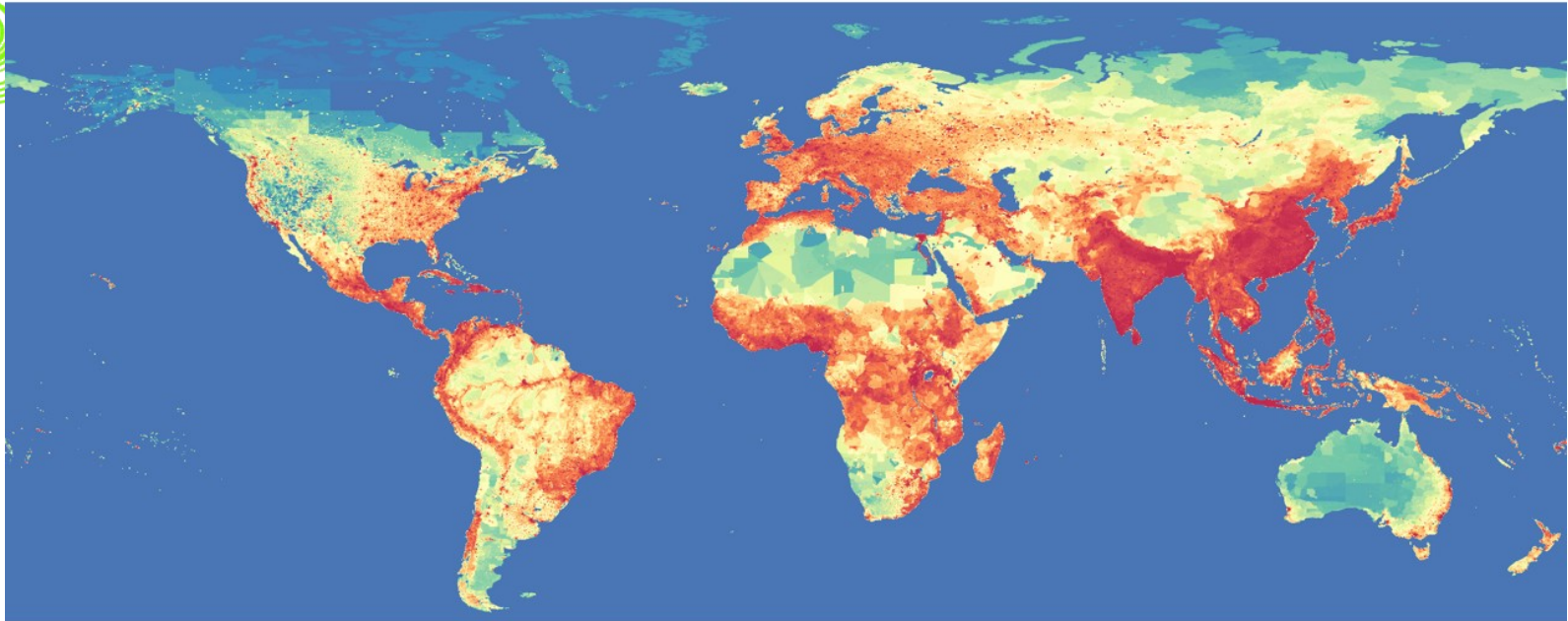
Local conservation.
Global health.



Temporal patterns in EID events

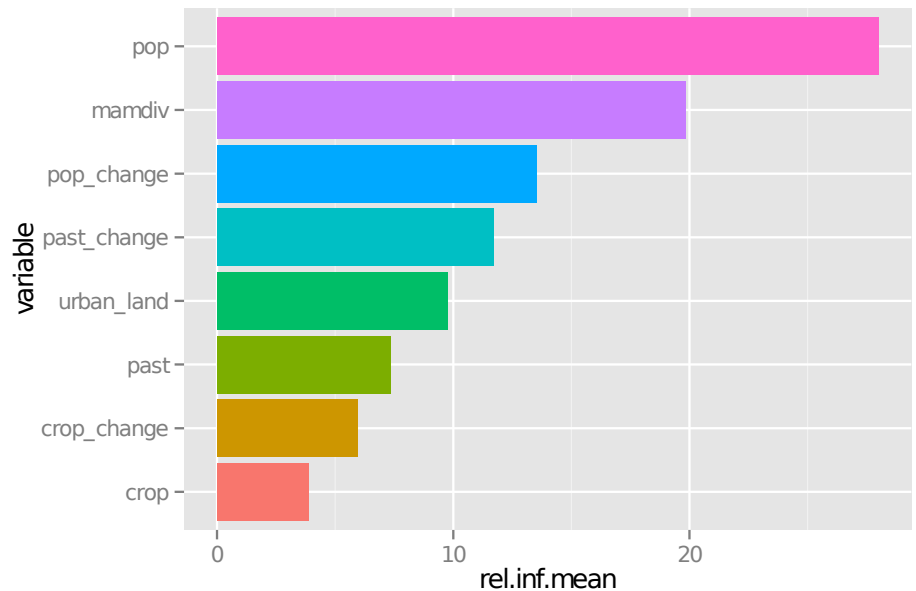


- EID events have increased over time, correcting for reporter bias ($\text{GLM}_{\text{P, JID}}$ $F = 86.4$, $p < 0.001$, $d.f. = 57$)
- ~5 new EIDs each year
- ~3 new Zoonoses each year
- **Zoonotic EIDs from wildlife** reach highest proportion in recent decade

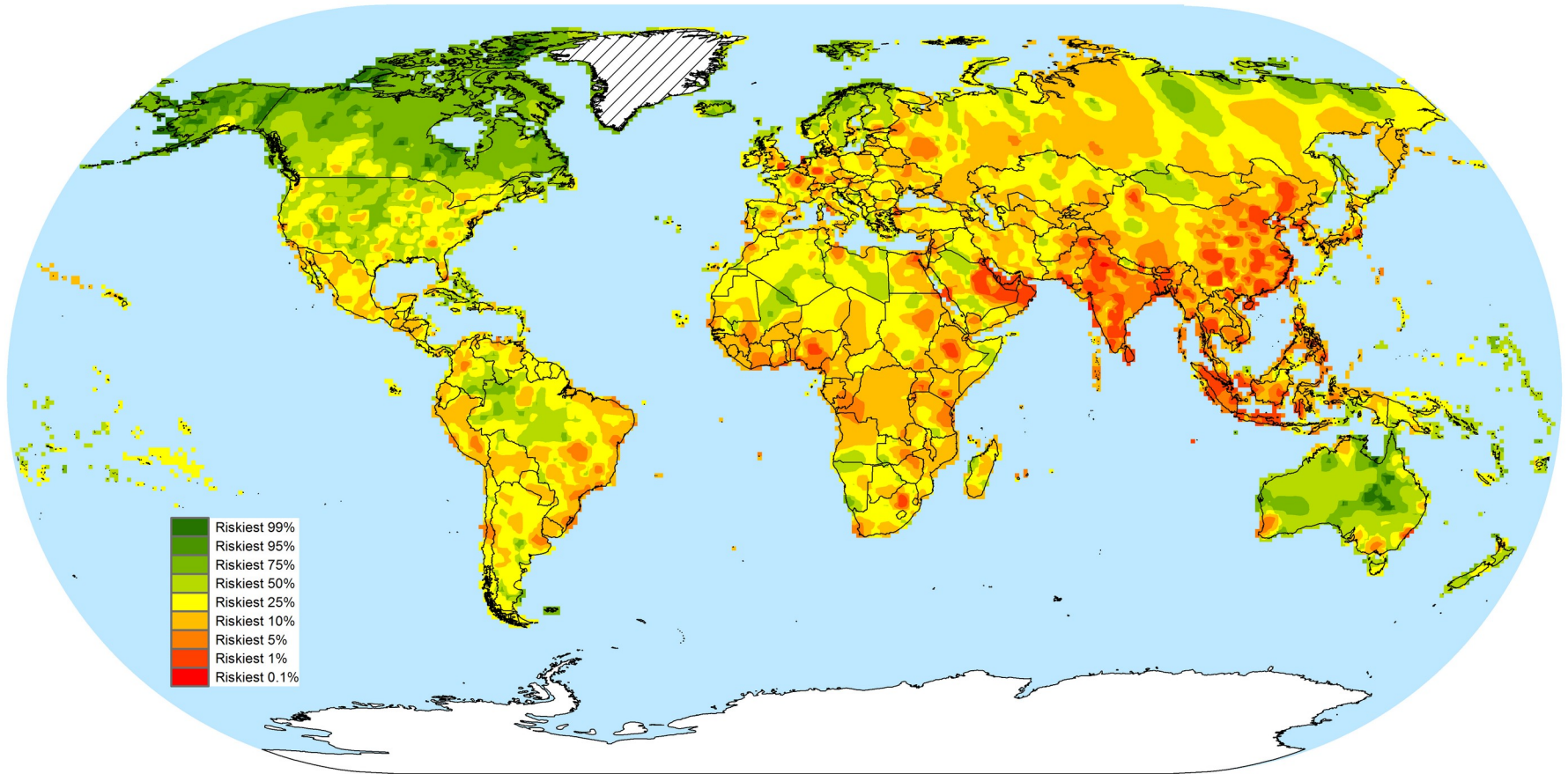


	relative influence (%)	std. dev.
population	27.99	2.99
mammal diversity	19.84	3.30
change: pop	13.54	1.54
change: pasture	11.71	1.30
urban extent	9.77	1.62

Local conservation.
Global health.



Global Vulnerability: Zoonotic EIDs

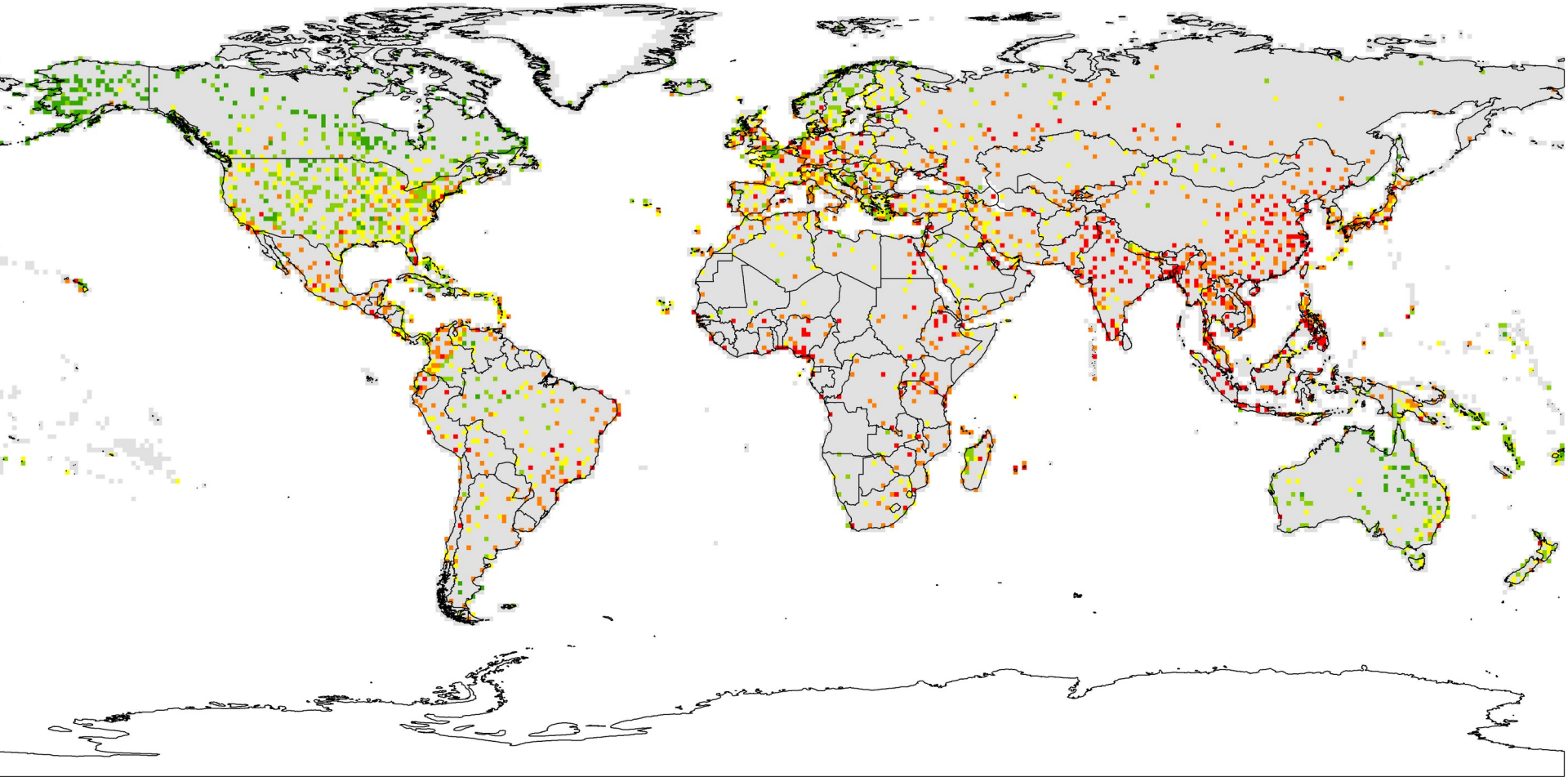


Hotspot risk + travel and trade out of a region



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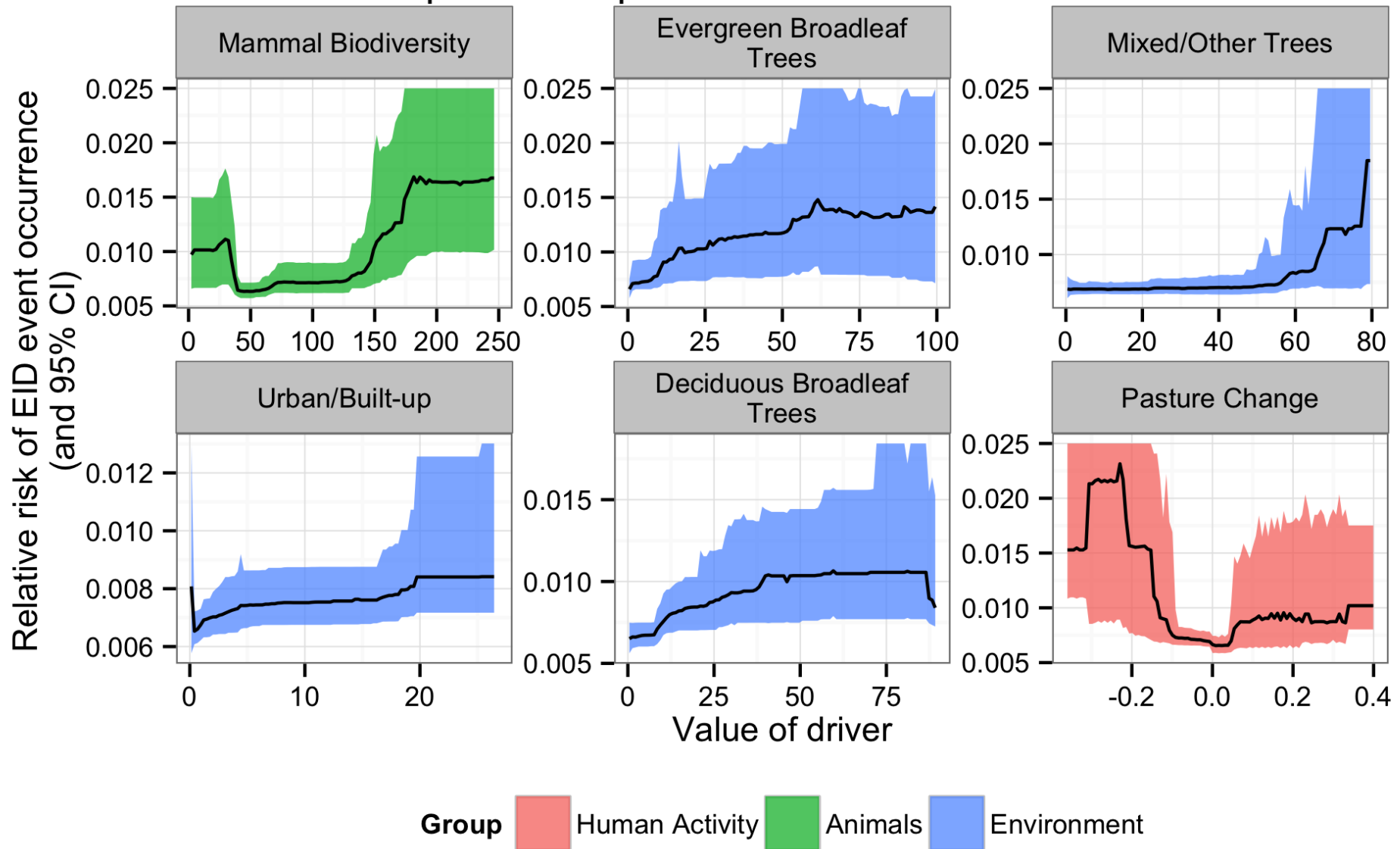
EID risk per airport



Local conservation.
Global health.

Hosseini *et al.* (in prep)

Partial dependence plot for zoonotic EID event occurrence



y-axis: relative probability of an EID event in a grid cell with this characteristic

x-axis: min. to max. values of each driver (except 'Pasture Change')

Plots show effect relative to human pop. Distribution, factoring out reporting



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Ground-truthing
hypotheses:
“DEEP FOREST” project

Borneo, Kinabatangan R.

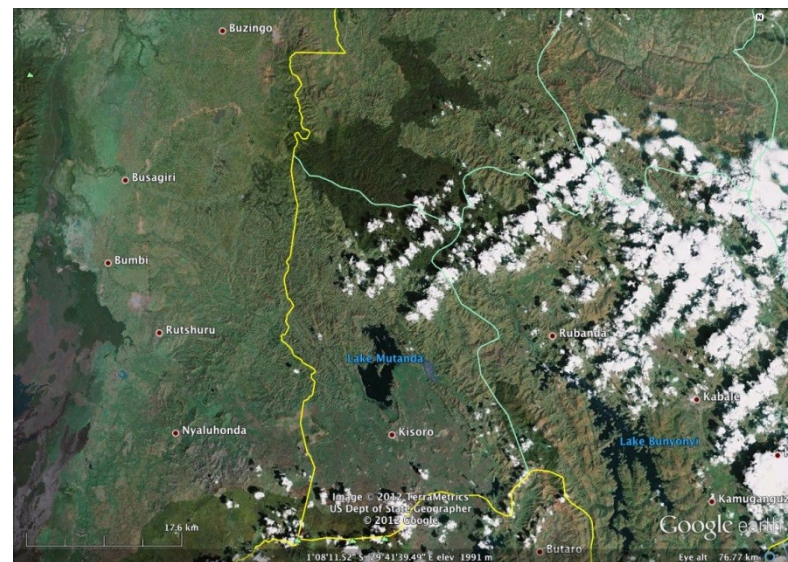


Brazil, Amazon basin



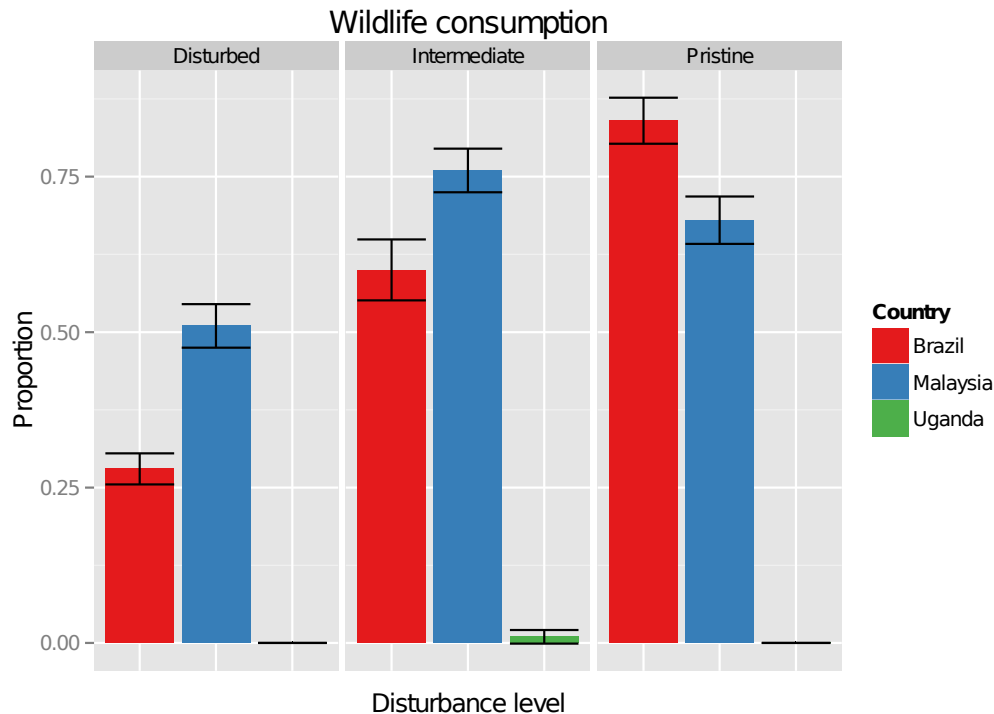
Global health.

Uganda, Bwindi Impenetrable Forest



Q1. Have you eaten any wildlife during the past year?

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Take homes:

- Eating wildlife is more common in more pristine areas.
- Overall difference in the proportion of people reporting eating wildlife between countries
- Significant interaction effect which suggests that this trend was not consistent across the gradient levels.

Table 1, Table of Deviance

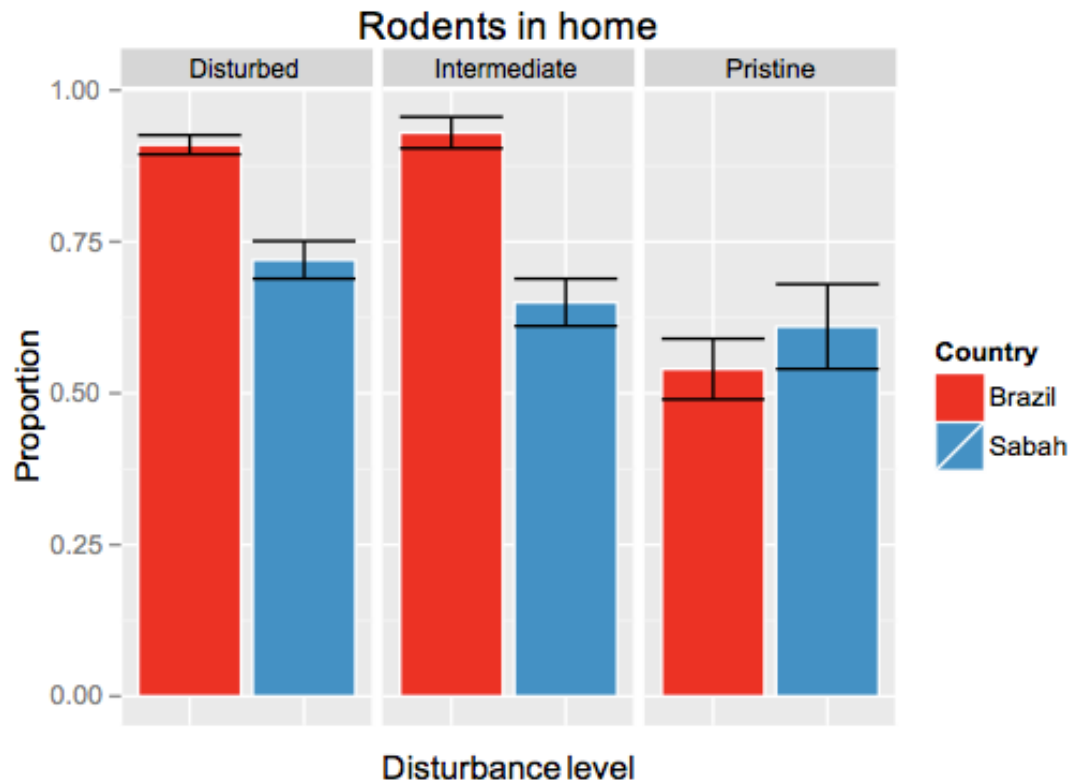
Term	Df	Dev Resid	Df	Resid Dev	p
NULL			840	1162.0	
Gradient	2	115.232	838	1046.8	***
Country	1	24.633	837	1022.1	***
Country*Gradient	2	12.896	835	1009.2	**

Note: The dependent variable is wildlife consumption coded so that 0 = Not in the last year and 1 = Sometime in the last year. Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q2. During the past year, have you seen rodents inside your home?



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Take homes:

- Rodents entering into the home is more common in more disturbed areas
- People in the disturbed and intermediate areas are more likely to report rodents coming into their homes than people in the pristine areas

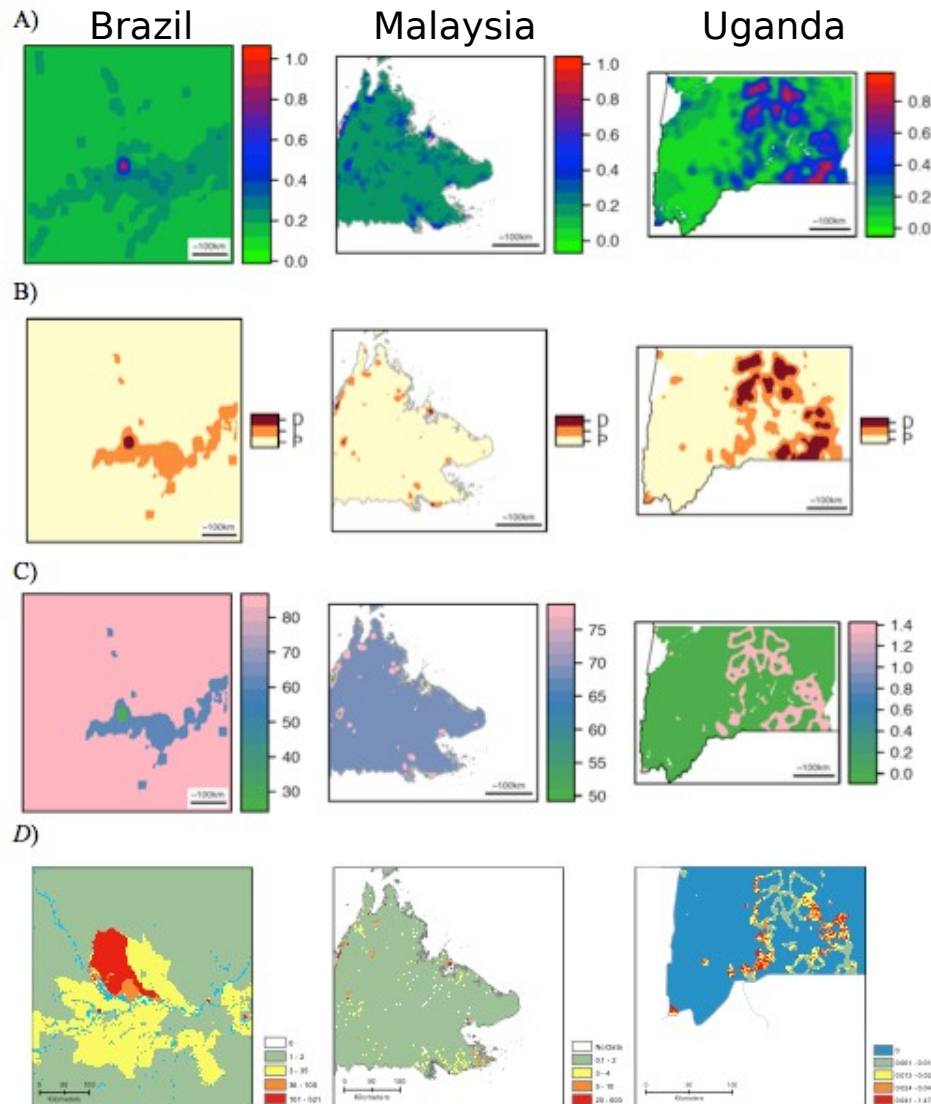
Table 3, Table of Deviance

Term	Df	Dev Resid	Df	Resid Dev	p
NULL			874	933.35	
Gradient	2	38.155	872	895.19	***
Country	1	43.348	871	851.84	***
Country*Gradient	2	14.952	869	836.89	***

Note: The dependent variable is whether a respondent reports wildlife coming into their home coded so that 0 = Never and 1 = Sometimes

DEEP FOREST: Mapping human-animal contact risk

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A) Land use change (raw LDI)

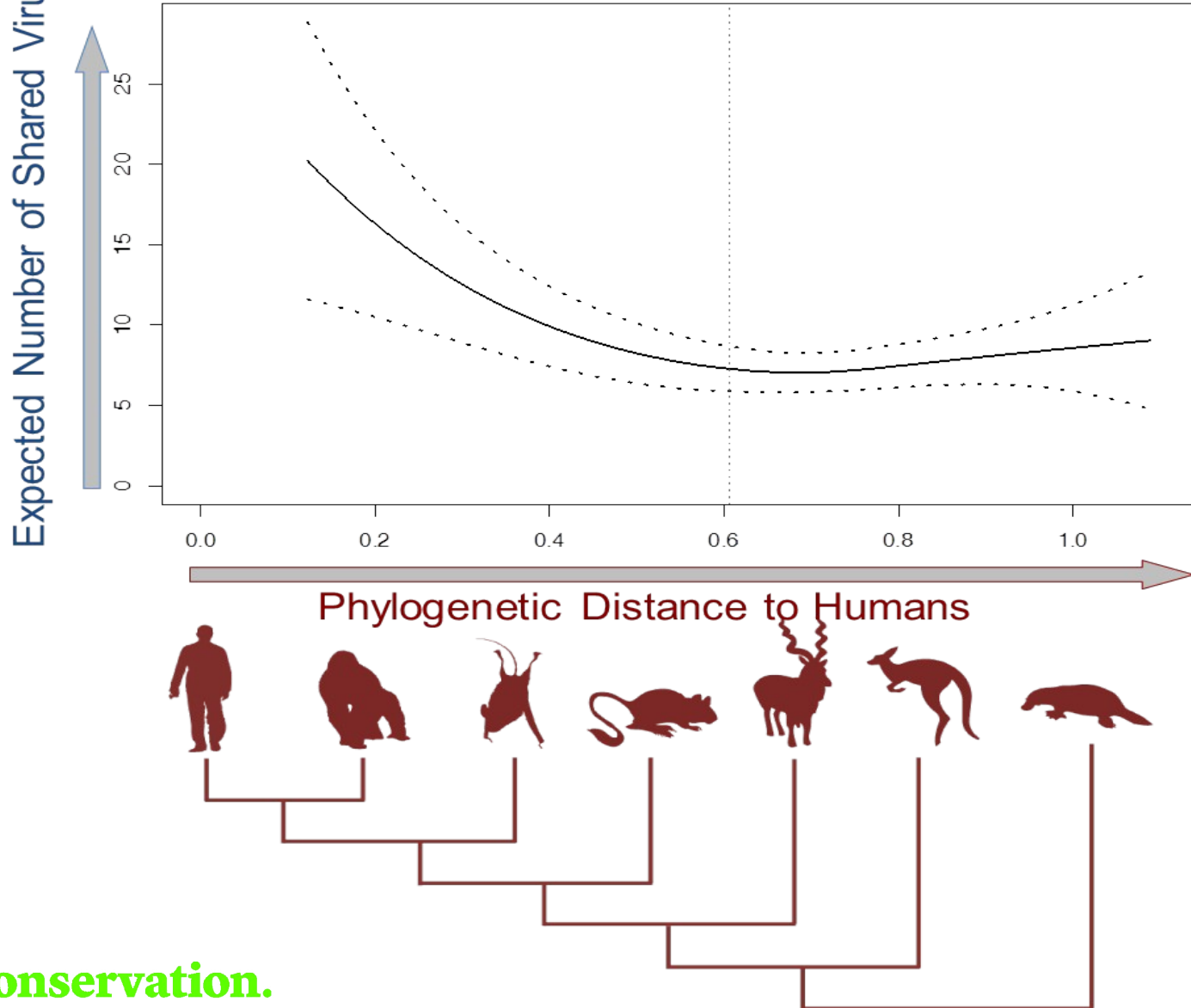
B) Reclassified LDI to match disturbance gradient levels

C) Wildlife consumption map from our DF surveys per gradient.

D) Map of relative human-animal contact risk (derived from proportion of people consuming wildlife x pop density)



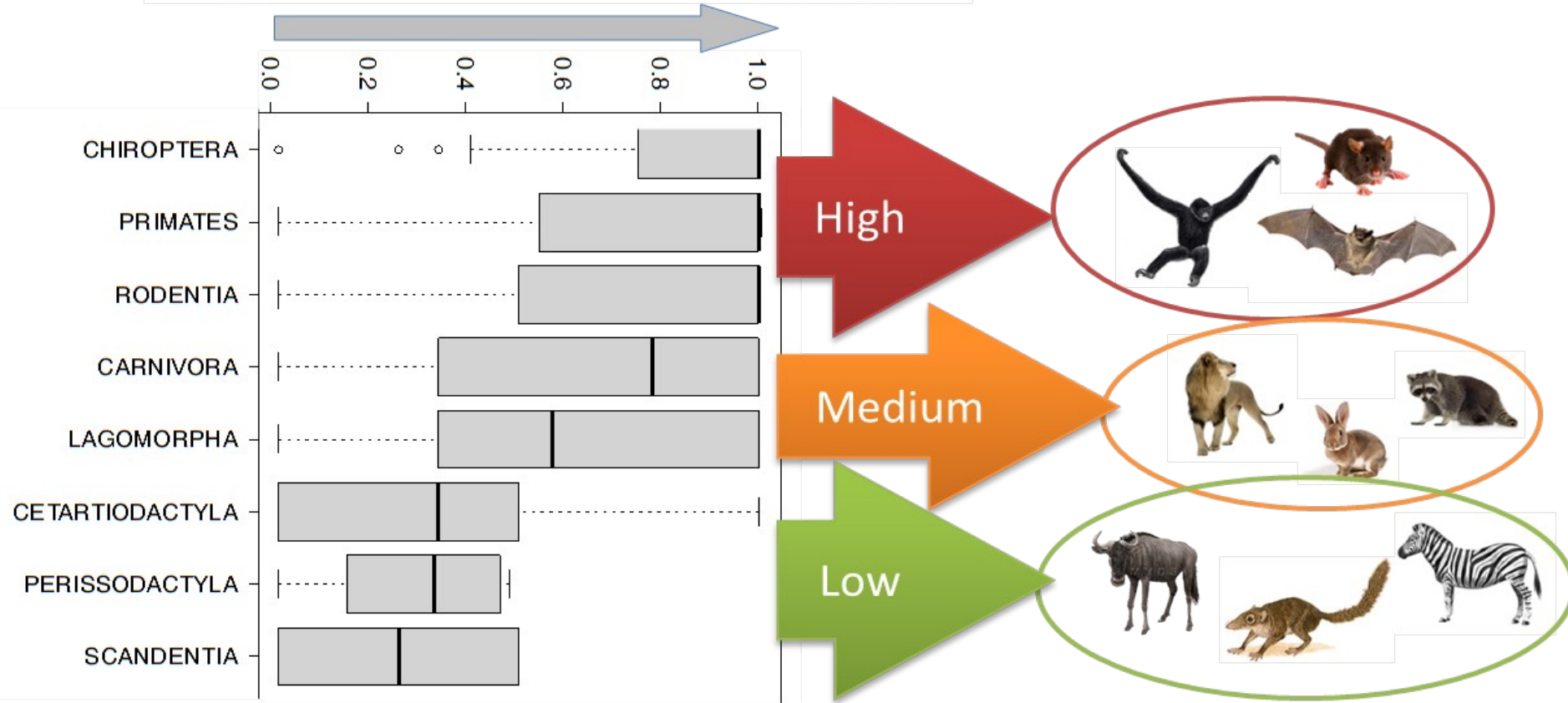
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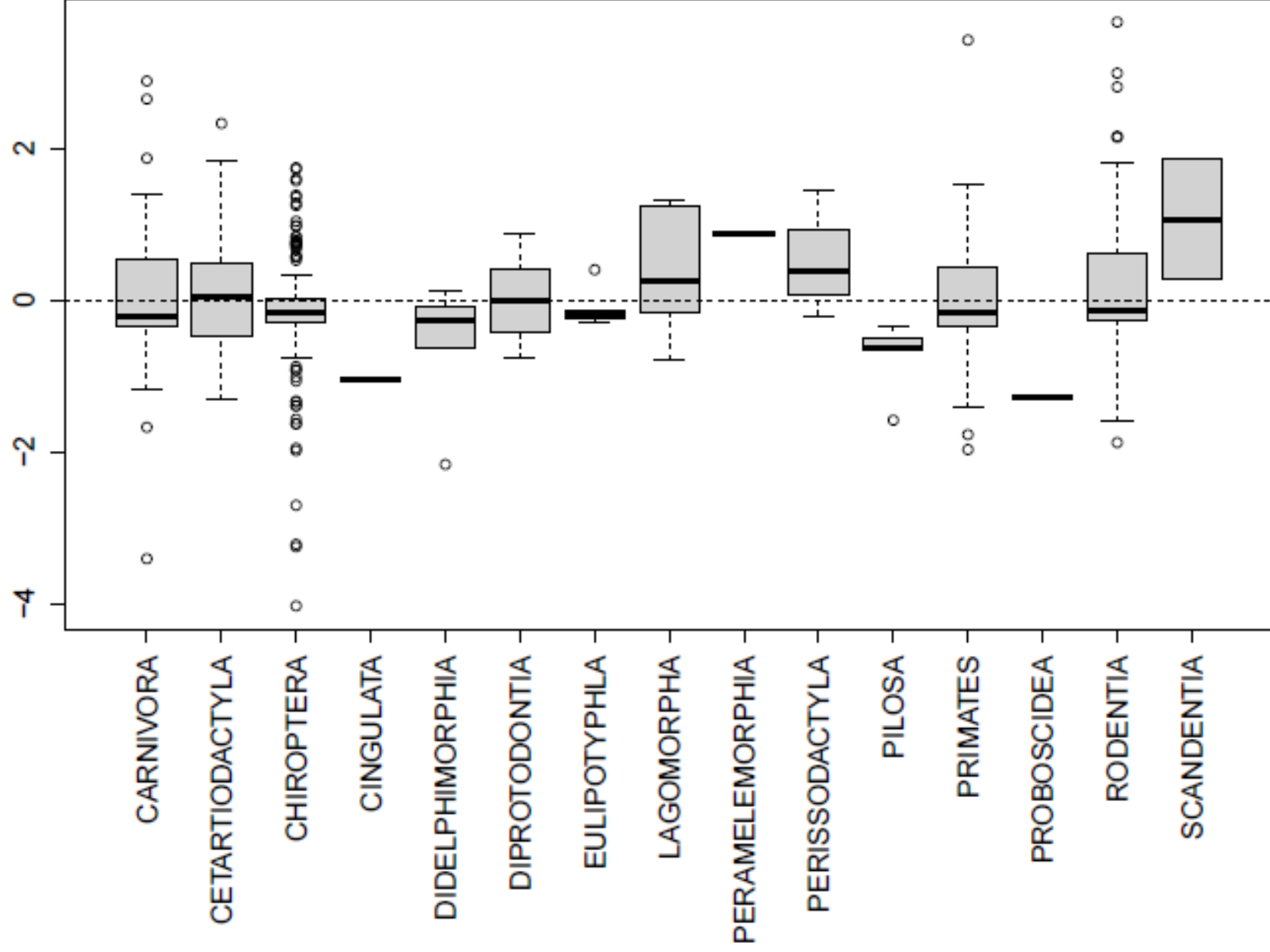
Which species will the next pandemic emerge from?

Proportion of viruses shared with humans



Local conservation.
Global health.

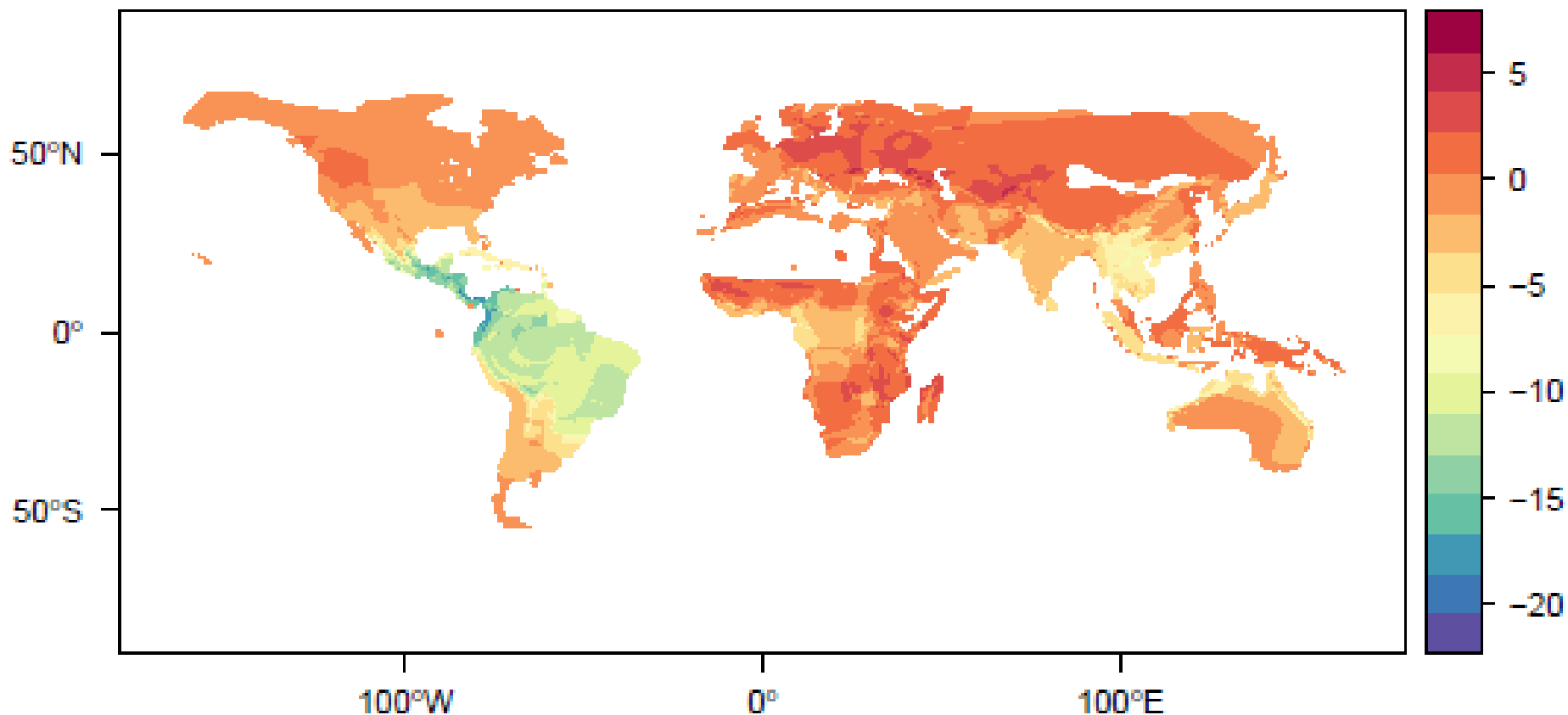
Model Residuals, Zoonotic Viruses per Species





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Bats: missing zoonoses



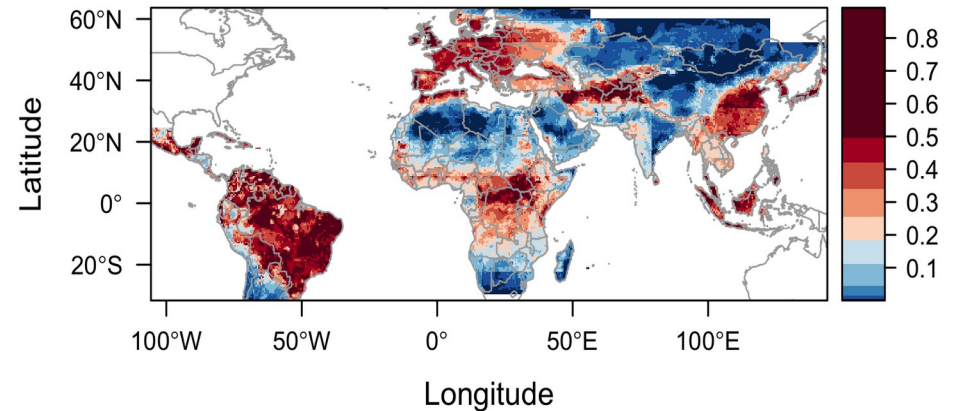
Local conservation.

Global health.

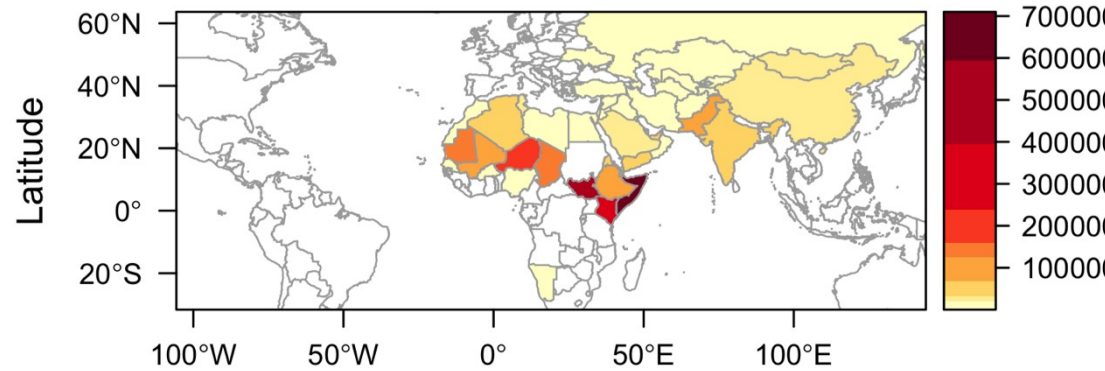
Where to look for specific pathogen groups



- Modeled distribution of MERS-CoV bats

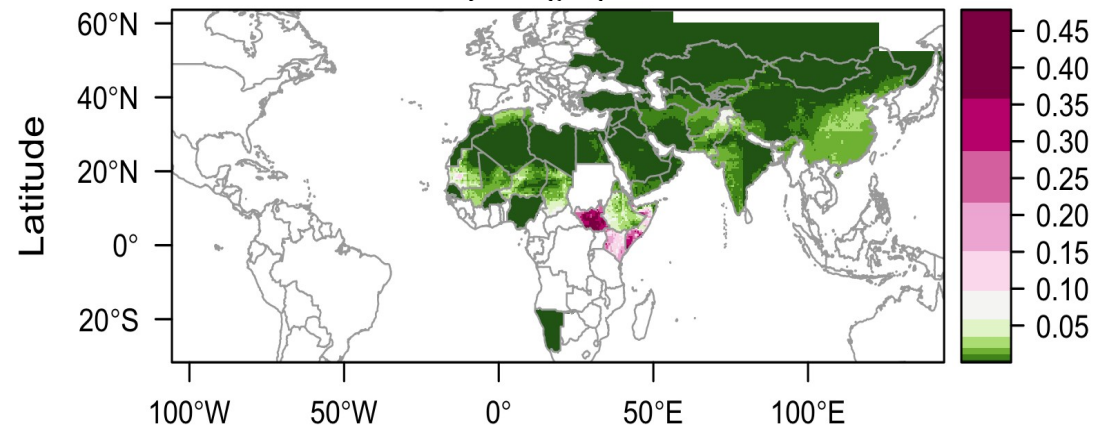


- Camel production (FAO)



- Modeled risk of MERS spillover (horn of Africa)

Local conservation.
Global health.





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The Great Donald Rumsfeld

“There are known knowns; there are things we know that we know.

There are known unknowns; that is to say, there are things that we now know we don't know.

But there are also unknown unknowns – there are things we do not know we don't know.”

US Secretary of Defense Donald Rumsfeld, Press briefing on links between Iraq and WMD, February 12, 2002

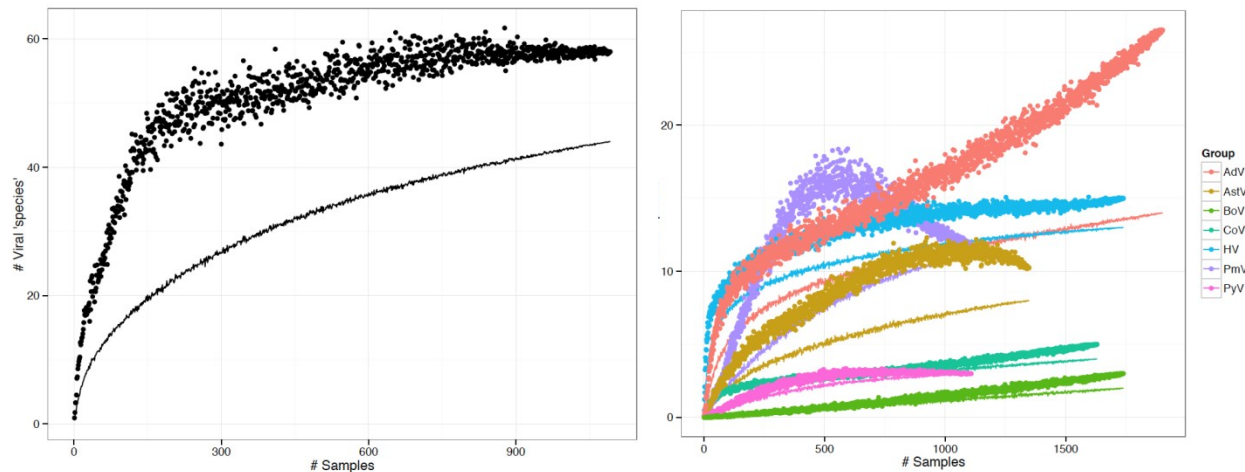


Local conservation.
Global health.

A Strategy To Estimate Unknown Viral Diversity in Mammals

Simon J. Anthony,^{a,b} Jonathan H. Epstein,^b Kris A. Murray,^b Isamara Navarrete-Macias,^a Carlos M. Zambrana-Torrel,^b Alexander Solovyov,^a Rafael Ojeda-Flores,^c Nicole C. Arrigo,^a Ariful Islam,^b Shahneaz Ali Khan,^d Parvize Hosseini,^b Tiffany L. Bogich,^{e,f} Kevin J. Olival,^b Maria D. Sanchez-Leon,^{a,b} William B. Karesh,^b Tracey Goldstein,^g Stephen P. Luby,^h Stephen S. Morse,^{g,i} Jonna A. K. Mazet,^g Peter Daszak,^b W. Ian Lipkin^a

Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, New York, USA^a; EcoHealth Alliance, New York, New York, USA^b; Facultad de Medicina Veterinaria and Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Mexico City, Distrito Federal, Mexico^c; Chittagong

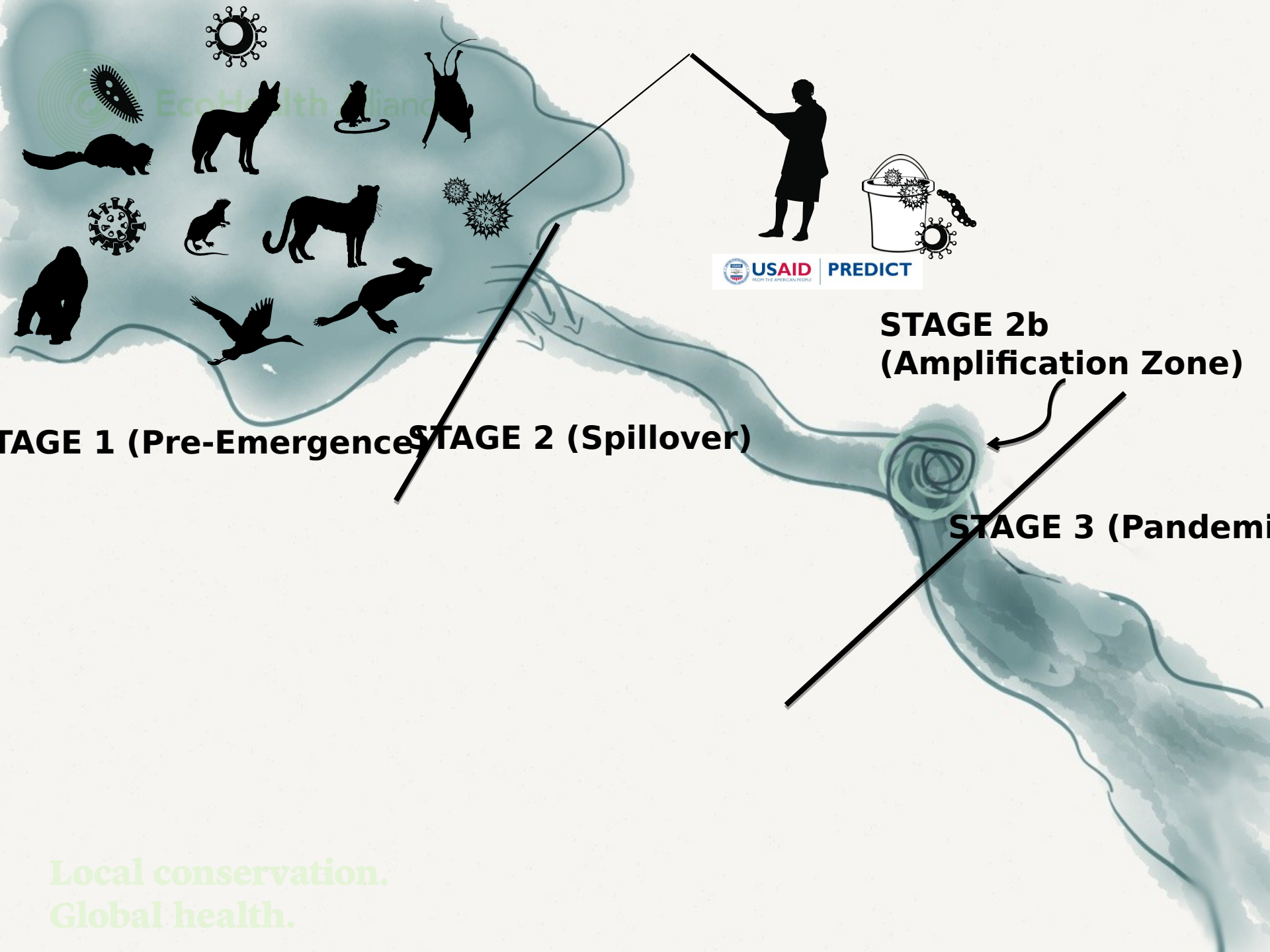


- ~58 unknown viruses in *Pteropus giganteus*
- ~320,000 unknown viruses in all mammals; ~72,152 in the 1,244 known bat species
- One-off cost to identify 100% = \$6.8 Billion
- One-off cost to identify 85% = \$1.4 Billion
- Cost of SARS = \$10-50 Billion

Local conservation
Global health. ~250 bat viruses in last 5 years, 530 total = 7% of the estimated
Anthony et al. *mBio* 2013



Local conservation.
Global health.



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USAID FROM THE AMERICAN PEOPLE PREDICT

STAGE 1 (Pre-Emergence)

STAGE 2 (Spillover)

STAGE 2b (Amplification Zone)

STAGE 3 (Pandemic)

Local conservation.
Global health.



Follow up Genetic and Experimental studies (post-PREDICT) to Further Assess Spillover Potential

- Virus isolation
- Sequence whole genome
- With temporally sampled viruses, measure mutation rates and phylodynamics
- Sequence receptor binding domain, if known
- Structural comparison with human receptors (e.g. 3D models, *In silico*)
- Cell line infection experiments (*in vitro*)
- Humanized mice and other animal experiments

With each step, increased risk possible

Local conservation.
Global health.

Increasing risk for zoonotic potential of novel viruses



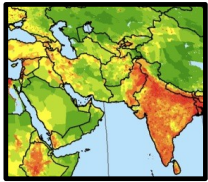
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**VIRUS-INDEPENDENT
TRAITS**

+

**VIRUS-SPECIFIC
TRAITS** =

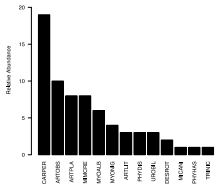
**RISK OF
SPILLOVER**



Geographic
hotspots for
emergence



Host species
traits, geographic
range,
relatedness



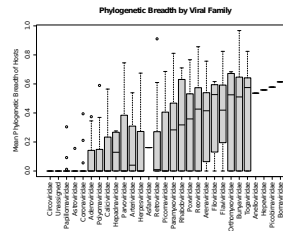
Host abundance

%
pos

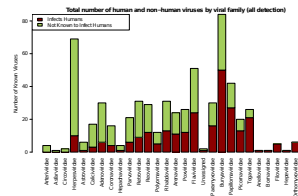
Viral prevalence
in host



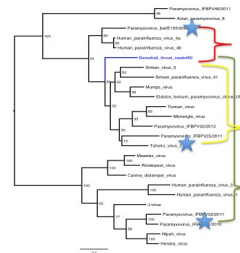
Epidemiological/
contract interface
on a global health.



Host
breadth/plasticity



Proportion
known zoonoses
in virus family



Phylogenetic
relatedness to
known zoonoses

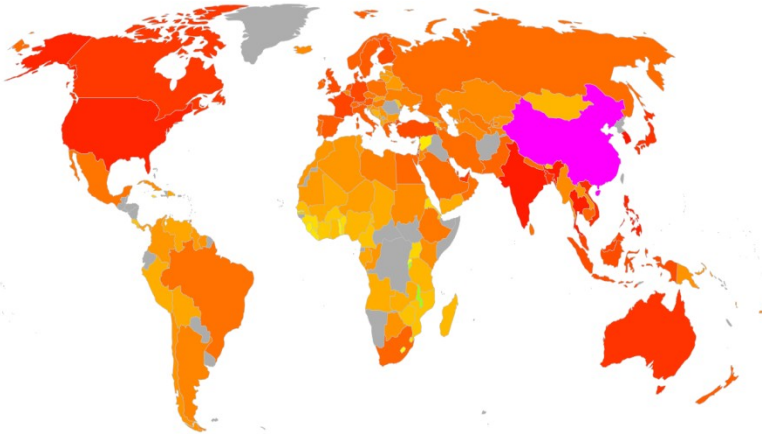


Other virus-
specific traits

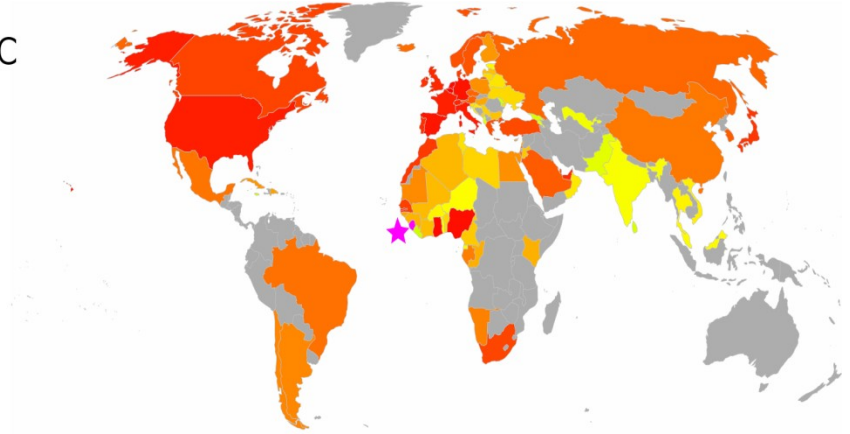


Where would a new virus travel to?

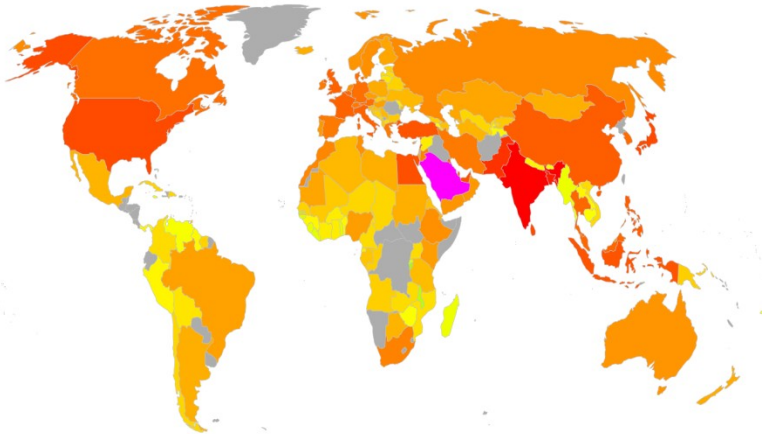
A



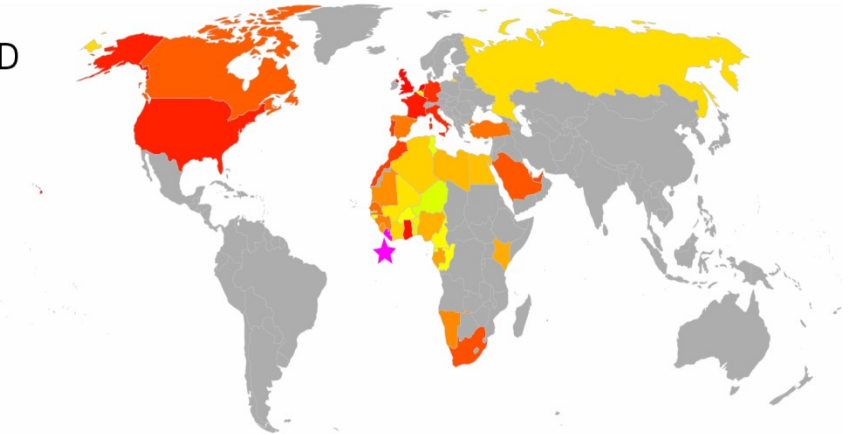
C



B



D



(A) Influenza A/H7N9, China; (B) MERS, S. Arabia; (C) Ebola virus, S. Leone; (D) Ebola, Liberia

Local conservation.

Global health.

Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li,^{1,2} Zhengli Shi,^{2*} Meng Yu,³ Wuze Ren,² Craig Smith,⁴ Jonathan H. Epstein,⁵ Hanzhong Wang,² Gary Crameri,³ Zhihong Hu,² Huajun Zhang,² Jianhong Zhang,² Jennifer McEachern,³ Hume Field,⁴ Peter Daszak,⁵ Bryan T. Eaton,³ Shuyi Zhang,^{1,6*} Lin-Fa Wang^{3*}

Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. These viruses, termed SARS-like coronaviruses (SL-CoV), display greater genetic variation than SARS-CoV isolated from humans or from civets. The human and civet isolates of SARS-CoV nestle phylogenetically within the spectrum of SL-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

survey bats in the search for the natural reservoir of SARS-CoV.

In this study, conducted from March to December of 2004, we sampled 408 bats representing nine species, six genera, and three families, from four locations in China (Guangdong, Guangxi, Hubei, and Tianjin) after trapping them in their native habitat (Table 1). Blood, fecal, and throat swabs were collected; serum samples and cDNA from fecal or throat samples were independently analyzed, double-blind, with different methods in Wuhan and Geelong (14).

Among six genera of bat species surveyed (*Rousettus*, *Cynopterus*, *Myotis*, *Rhinolophus*, *Nyctalus*, and *Miniopterus*), three communal, cave-dwelling species from the genus *Rhinolophus* (horseshoe bats) in the family *Rhinolophidae* demonstrated a high SARS-CoV antibody prevalence: 13 out of 46 bats (28%) in *R. pearsoni* from Guangxi, 2 out of 6 bats (33%) in *R. pusillus* from Guangxi; and 5 out

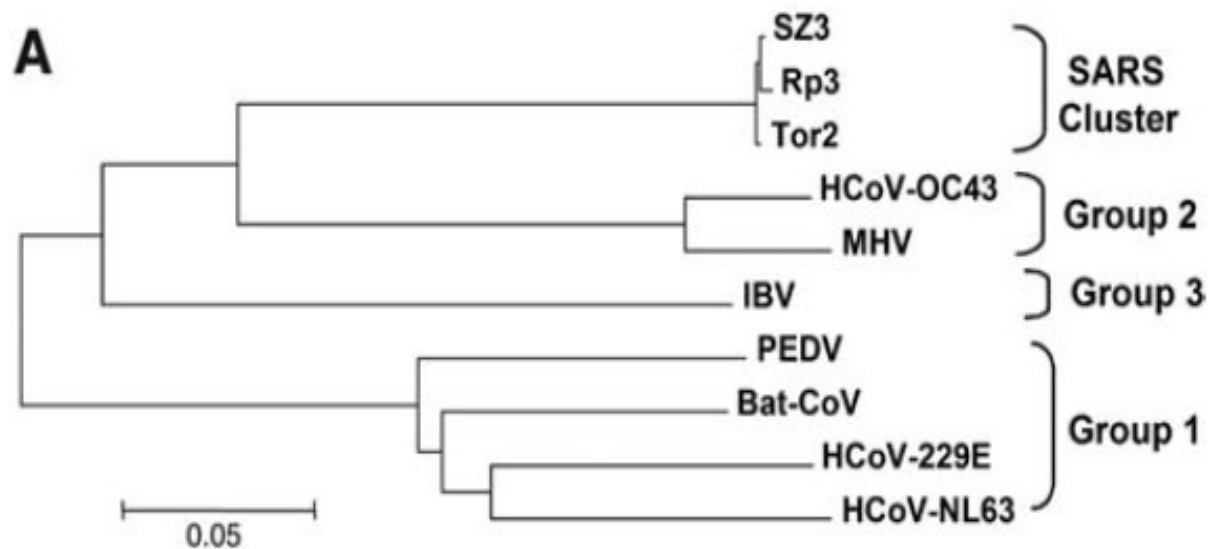


Human and Civet SARS-CoV nestle phylogenetically within Bat SL-CoV cluster

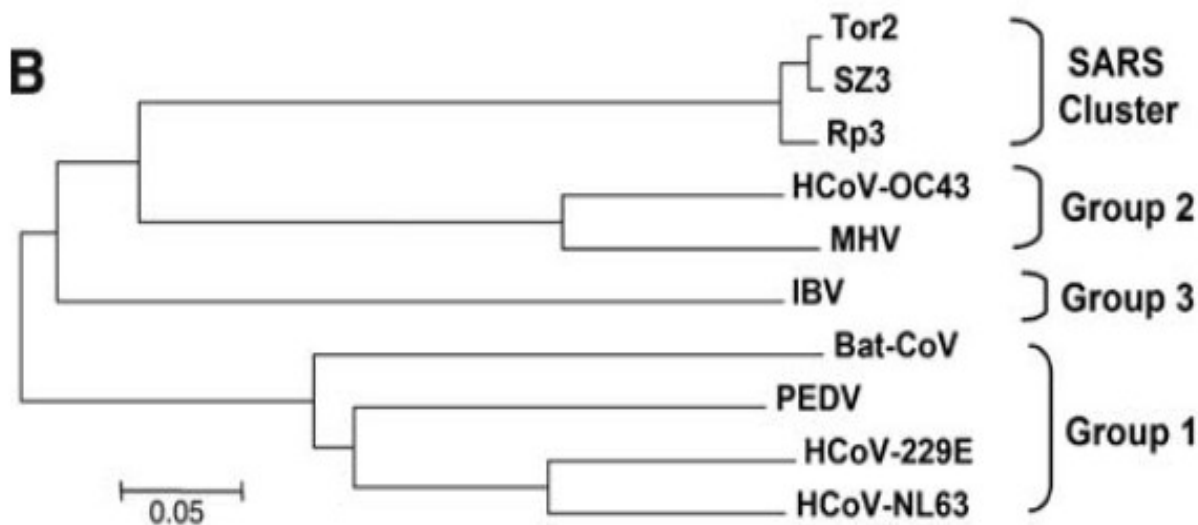


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SL-CoV cluster



P1b



S

Local cons
Global health.

Li *et al.* Science 2005



Human SARS CoV Tor2
Human SARS CoV BJ01
Human SARS CoV GZ02
Civet SARS CoV SZ3

Bat SL-CoV Rs_4087-1

Bat SL-CoV Rs_4110

Bat SL-CoV Rs_4090

Bat SL-CoV Rs_4079

Bat SL-CoV Rs_3367

Bat SL-CoV Rs_4105

Bat SL-CoV Rs_SHC012*

Bat SL-CoV Rs_4084

Bat SL-CoV Rs_3267-1

Bat SL-CoV Rs_3262-1

Bat SL-CoV Rs_3369*

Bat SL-CoV Rf1

Bat SL-CoV Rs_4075

Bat SL-CoV Rs_4092

Bat SL-CoV Rs_4085

Bat SL-CoV Rs_3262-2

Bat SL-CoV Rs_3267-2

Bat SL-CoV HKU3-1

Bat SL-CoV Rm1

Bat SL-CoV Rp3

Bat SL-CoV Rs_4108

Bat SL-CoV Rs672

Bat SL-CoV Rs_4081

Bat SL-CoV Rs_4096

Bat SL-CoV Rs_4087-2

Bat SL-CoV Rs_4097

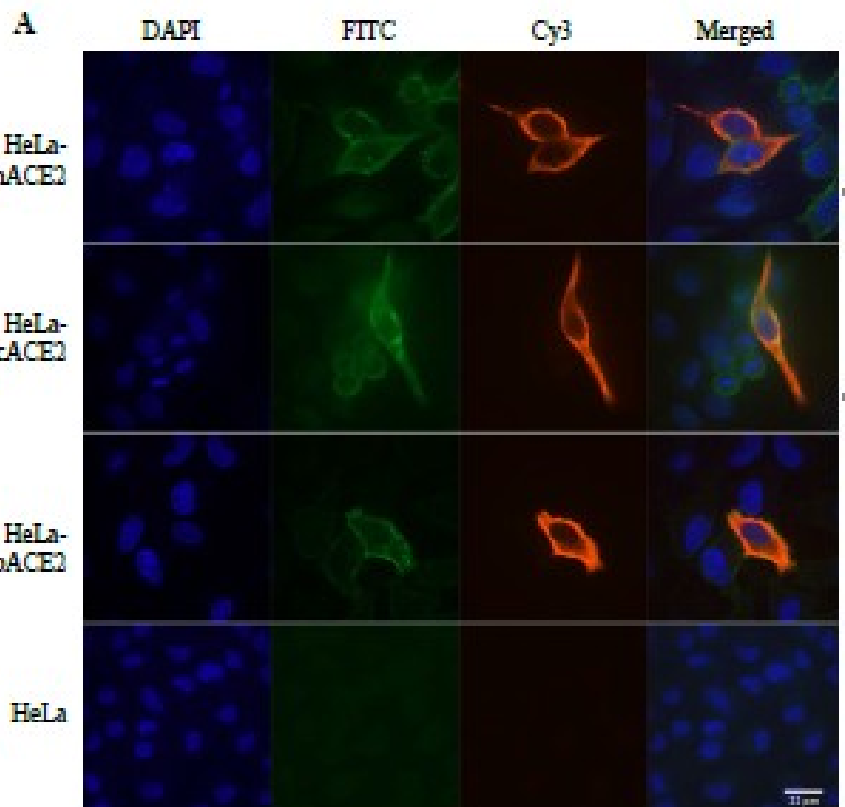
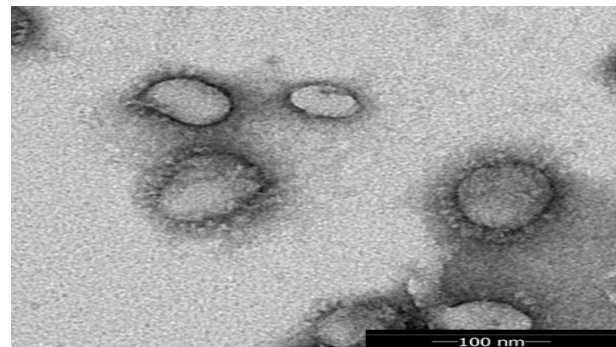
Bat SL-CoV Rs_4080

Bat SARS-related CoV BM48

Bat CoV HKU9-1

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Global health.



Ge et al. (2013) Nature

Global Rapid Identification Tool (GRITS)

- Automated diagnosis from online feeds
- Validated via Amazon Mechanical Turk

MANTLE

Web platform built for the One Health community to collect, share, and visualize information from human, animal, and environmental health.

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Global health.

Emerging Infectious Disease Repository (EIDR)



Centralized web-application dedicated to the improvement, storage, display, dissemination, and discussion of current knowledge on historical disease emergence.

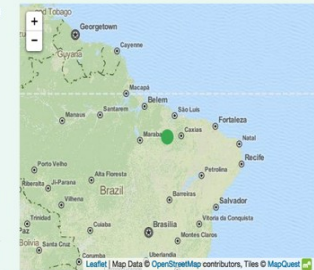


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Anajatuba virus

March 2000

In May 2000, a 19 year old female student was home. She was helping her parents with field work in a rural village in Anajatuba, Brazil. On May 20, this young student became seriously ill, presenting with a fever of 39 °C, shivering, intense generalized myalgia predominating in the lumbar region, persistent dry cough. She was treated with diclofenac and gentamicin, but developed intense dyspnea, cyanotic extremities, tachycardia and profuse diarrhea. She died shortly after being transferred to a hospital in São Luís. Serological testing confirmed infection by a novel sub-species of hantavirus and a diagnosis of hantavirus pulmonary syndrome (HPS). Two suspected cases occurred within 8 miles of the confirmed case, in two men of first-degree relation, ages 19 and 25 respectively. Rodents are a known host for HPS and transmission occurs by, "inhalation of aerosols containing the virus, by contact with a rodent's saliva during a bite, or by contact of non-intact skin with rodent excreta" (Mendes et al. 2001). A serious rodent infestation occurred during the time of these outbreaks, which may have been caused by seasonal flooding. It is likely that this infestation, coupled with the storage of rice and corn within the households of all three cases, facilitated infection. In this outbreak, the emergence of HPS developed in a new region.



Maranhão, Brazil
This represents the most specific location information found for the event.

Emergence Type	Driver	Disease
New Region, Evolution an existing organism	Human Behavior, Climate and Weather, Ecosystem Change	Hantavirus pulmonary syndrome
Event Transmission	Pathogen Host(s)	Specific Host Involved in the Event
	Rodents	Rodent



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Collaborators

- UC Davis, Metabiota, WCS, Smithsonian
- Univ. Wyoming (David Finnoff)
- Columbia Univ. (Ian Lipkin, Simon Anthony)
- 100+ partners in 24 countries
- Wuhan Institute of Virology, Yunnan C
- Universiti Malaysia Sabah, Sabah Wildlife Dept

Funders



USAID
FROM THE AMERICAN PEOPLE



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Conservation Medicine • Human Health • Ecosystem Sustainability

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